

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
- (ii) TITLE OF INVENTION: Patched Genes and their Use
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 - (B) STREET: Four Embarcadero Center, Suite 3400
 - (C) CITY: San Francisco
 - (D) STATE: CA
 - (E) COUNTRY: US
 - (F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: PCT/US95/
 - (B) FILING DATE: 06-OCT-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Rowland, Bertram I
 - (B) REGISTRATION NUMBER: 20015
 - (C) REFERENCE/DOCKET NUMBER: a60190-1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 415-781-1989
 - (B) TELEFAX: 415-398-3249

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACNNC NNTN NATGGCACCC CCNCCCAACC TTTNNNCCNN NTAANCAAAA NNCCCCNTTT

60

NATACCCCT NTAAANTTT TCCACNNNC NNAAANNCCN CTGNANACNA NGNAAANCCN 120
 TTTTNAACC CCCCCACCC GGAATTCNA NTNNCCNCCC CCAAATTACA ACTCCAGNCC 180
 AAAATTNANA NAATTGGTCC TAACCTAACC NATNGTTGTT ACGGTTTCCC CCCCCAAATA 240
 CATGCACTGG CCCGAACACT TGATCGTTGC CGTTCCAATA AGAATAAATC TGGTCATATT 300
 AAACAAGCCN AAAGCTTTAC AACTGTTGT ACAATTAATG GCGAACACG AACTGTTTGA 360
 ATTCTGGTCT GGACATTACA AAGTGACCA CATCGGATGG AACCAGGAGA AGGCCACAAC 420
 CGTACTGAAC GCCTGGCAGA AGAAGTTCGC ACAGGTTGGT GGTGGCGCA AGGAGTAGAG 480
 TGAATGGTGG TAATTTTTGG TTGTTCCAGG AGGTGGATCG TCTGACGAAG AGCAAGAAGT 540
 CGTCGAATTA CATCTTCGTG ACGTTCTCCA CCGCCAATTT GAACAAGATG TTGAAGGAGG 600
 CGTCGAANAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG GTGTACGGGT 660
 GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTNGCGNGC TNCNATTCGC 720
 CCTATAGTNA GNCGTA 736

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Pro	Pro	Pro	Asn	Tyr	Asn	Ser	Xaa	Pro	Lys	Xaa	Xaa	Xaa	Leu	Val
1				5				10						15	
Leu	Thr	Pro	Xaa	Val	Val	Thr	Val	Ser	Pro	Pro	Lys	Tyr	Met	His	Trp
			20					25					30		
Pro	Glu	His	Leu	Ile	Val	Ala	Val	Pro	Ile	Arg	Ile	Asn	Leu	Val	Ile
		35				40					45				
Leu	Asn	Lys	Pro	Lys	Ala	Leu	Gln	Thr	Val	Val	Gln	Leu	Met	Gly	Glu
	50				55					60					
His	Glu	Leu	Phe	Glu	Phe	Trp	Ser	Gly	His	Tyr	Lys	Val	His	His	Ile
65				70				75						80	
Gly	Trp	Asn	Gln	Glu	Lys	Ala	Thr	Thr	Val	Leu	Asn	Ala	Trp	Gln	Lys
			85					90						95	
Lys	Phe	Ala	Gln	Val	Gly	Gly	Trp	Arg	Lys	Glu					

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCTGTCA CCCGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC	60
CCAGGCGCGC CCGGAGCCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC	120
GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC	180
GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG	240
GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG	300
TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG	360
GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG	420
ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT	480
ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA	540
AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGA CTCAGCA	600
CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG	660
TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC	720
CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGAAGGGGC AAAGCTACAG	780
TCCGGGACAG CATACTCCT AGGTAAGCCT CCTTTACGGT GGACAACTT TGACCCCTTG	840
GAATTCCTAG AAGAGTTAAA GAAATAAAC TACCAAGTGG ACAGCTGGA GGAAATGCTG	900
AATAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA	960
GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT	1020
TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT	1080
GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAAGTTGTCA GCGCTCACGC CCTGCAAACC	1140
ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC	1200
TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT	1260

TACGTGGAGG	TGGTTCATCA	AAGTGTGCGC	CCAAACTCCA	CTCAAAAGGT	GCTTCCCTTC	1320
ACAACCACGA	CCCTGGACGA	CATCCTAAAA	TCCTTCTCTG	ATGTCAGTGT	CATCCGAGTG	1380
GCCAGCGGCT	ACCTACTGAT	GCTTGCCTAT	GCCTGTTTAA	CCATGCTGCG	CTGGGACTGC	1440
TCCAAGTCCC	AGGGTGCCGT	GGGGCTGGCT	GGCGTCCTGT	TGGTTGCGCT	GTCAGTGGCT	1500
GCAGGATTGG	GCCTCTGCTC	CTTGATTGGC	ATTTCTTTTA	ATGCTGCGAC	AACTCAGGTT	1560
TTGCCGTTTC	TTGCTCTTGG	TGTTGGTGTG	GATGATGTCT	TCCTCCTGGC	CCATGCATTC	1620
AGTGAAACAG	GACAGAATAA	GAGGATTCCA	TTTGAGGACA	GGACTGGGGA	GTGCCTCAAG	1680
CGCACCGGAG	CCAGCGTGGC	CCTCACCTCC	ATCAGCAATG	TCACCGCCTT	CTTCATGGCC	1740
GCATTGATCC	CTATCCCTGC	CCTGCGAGCG	TTCTCCCTCC	AGGCTGCTGT	GGTGGTGGTA	1800
TTCAATTTTG	CTATGGTTCT	GCTCATTTTT	CCTGCAATTC	TCAGCATGGA	TTTATACAGA	1860
CGTGAGGACA	GAAGATTGGA	TATTTTCTGC	TGTTTCACAA	GCCCCTGTGT	CAGCAGGGTG	1920
ATTCAAGTTG	AGCCACAGGC	CTACACAGAG	CCTCACAGTA	ACACCCGGTA	CAGCCCCCCA	1980
CCCCCATACA	CCAGCCACAG	CTTCGCCCAC	GAAACCCATA	TCACTATGCA	GTCCACCGTT	2040
CAGCTCCGCA	CAGAGTATGA	CCCTCACACG	CACGTGTACT	ACACCACCGC	CGAGCCACGC	2100
TCTGAGATCT	CTGTACAGCC	TGTTACCGTC	ACCCAGGACA	ACCTCAGCTG	TCAGAGTCCC	2160
GAGAGCACCA	GCTCTACCAG	GGACCTGCTC	TCCCAGTTCT	CAGACTCCAG	CCTCCACTGC	2220
CTCGAGCCCC	CCTGCACCAA	GTGGACACTC	TCTTCGTTTG	CAGAGAAGCA	CTATGCTCCT	2280
TTCTCTCTGA	AACCCAAAGC	CAAGGTTGTG	GTAATCCTTC	TTTTCTGGG	CTTGCTGGGG	2340
GTCAGCCTTT	ATGGGACCAC	CCGAGTGAGA	GACGGGCTGG	ACCTCACGGA	CATTGTTCCC	2400
CGGGAAACCA	GAGAATATGA	CTTCATAGCT	GCCCAGTTCA	AGTACTTCTC	TTTCTACAAC	2460
ATGTATATAG	TCACCCAGAA	AGCAGACTAC	CCGAATATCC	AGCACCTACT	TTACGACCTT	2520
CATAAGAGTT	TCAGCAATGT	GAAGTATGTC	ATGCTGGAGG	AGAACAAGCA	ACTTCCCCAA	2580
ATGTGGCTGC	ACTACTTTAG	AGACTGGCTT	CAAGGACTTC	AGGATGCATT	TGACAGTGAC	2640
TGGGAAACTG	GGAGGATCAT	GCCAAACAAT	TATAAAAATG	GATCAGATGA	CGGGGTCTTC	2700
GCTTACAAAC	TCCTGGTGCA	GACTGGCAGC	CGAGACAAGC	CCATCGACAT	TAGTCAGTTG	2760
ACTAAACAGC	GTCTGGTAGA	CGCAGATGGC	ATCATTAATC	CGAGCGCTTT	CTACATCTAC	2820
CTGACCGCTT	GGGTCAGCAA	CGACCCTGTA	GCTTACGCTG	CCTCCCAGGC	CAACATCCGG	2880
CCTCACCGGC	CGGAGTGGGT	CCATGACAAA	GCCGACTACA	TGCCAGAGAC	CAGGCTGAGA	2940
ATCCCAGCAG	CAGAGCCCAT	CGAGTACGCT	CAGTTCCCTT	TCTACCTCAA	CGGCCTACGA	3000

GACACCTCAG	ACTTTGTGGA	AGCCATAGAA	AAAGTGAGAG	TCATCTGTAA	CAACTATACG	3060
AGCCTGGGAC	TGTCCAGCTA	CCCCAATGGC	TACCCCTTCC	TGTTCTGGGA	GCAATACATC	3120
AGCCTGCGCC	ACTGGCTGCT	GCTATCCATC	AGCGTGGTGC	TGGCCTGCAC	GTTTCTAGTG	3180
TGCGCAGTCT	TCCTCCTGAA	CCCCTGGACG	GCCGGGATCA	TTGTCATGGT	CCTGGCTCTG	3240
ATGACCGTTG	AGCTCTTTGG	CATGATGGGC	CTCATTTGGA	TCAAGCTGAG	TGCTGTGCCT	3300
GTGGTCATCC	TGATTGCATC	TGTTGGCATC	GGAGTGGAGT	TCACCGTCCA	CGTGGCTTTG	3360
GCCTTTCTGA	CAGCCATTGG	GGACAAGAAC	CACAGGGCTA	TGCTCGCTCT	GGAACACATG	3420
TTTGCTCCCG	TTCTGGACGG	TGCTGTGTCC	ACTCTGCTGG	GTGTACTGAT	GCTTGCAGGG	3480
TCCGAATTTG	ATTTTATTGT	CAGATACTTC	TTTGCCGTCC	TGGCCATTCT	CACCGTCTTG	3540
GGGGTTCTCA	ATGGACTGGT	TCTGCTGCCT	GTCCTCTTAT	CCTTCTTTGG	ACCGTGTCCCT	3600
GAGGTGTCTC	CAGCCAATGG	CCTAAACCGA	CTGCCCACTC	CTTCGCCTGA	GCCGCCTCCA	3660
AGTGTGCTCC	GGTTTGCCGT	GCCTCCTGGT	CACACGAACA	ATGGGTCTGA	TTCCTCCGAC	3720
TCGGAGTACA	GCTCTCAGAC	CACGGTGTCT	GGCATCAGTG	AGGAGCTCAG	GCAATACGAA	3780
GCACAGCAGG	GTGCCGGAGG	CCCTGCCCAC	CAAGTGATTG	TGGAAGCCAC	AGAAAACCCT	3840
GTCTTTGCCC	GGTCCACTGT	GGTCCATCCG	GACTCCAGAC	ATCAGCCTCC	CTTGACCCCT	3900
CGGCAACAGC	CCCACCTGGA	CTCTGGCTCC	TTGTCCCCTG	GACGGCAAGG	CCAGCAGCCT	3960
CGAAGGGATC	CCCCTAGAGA	AGGCTTGCGG	CCACCCCCCT	ACAGACCGCG	CAGAGACGCT	4020
TTTGAAATTT	CTACTGAAGG	GCATTCTGGC	CCTAGCAATA	GGGACCGCTC	AGGGCCCCGT	4080
GGGGCCCCGT	CTCACAACCC	TCGGAACCCA	ACGTCCACCG	CCATGGGCAG	CTCTGTGCCC	4140
AGCTACTGCC	AGCCCATCAC	CACTGTGACG	GCTTCTGCTT	CGGTGACTGT	TGCTGTGCAT	4200
CCCCCGCCTG	GACCTGGGCG	CAACCCCCGA	GGGGGGCCCT	GTCCAGGCTA	TGAGAGCTAC	4260
CCTGAGACTG	ATCACGGGGT	ATTTGAGGAT	CCTCATGTGC	CTTTTCATGT	CAGGTGTGAG	4320
AGGAGGGACT	CAAAGGTGGA	GGTCATAGAG	CTACAGGACG	TGGAATGTGA	GGAGAGGCCG	4380
TGGGGGAGCA	GCTCCAACCTG	AGGGTAATTA	AAATCTGAAG	CAAAGAGGCC	AAAGATTGGA	4440
AAGCCCCGCC	CCCACCTCTT	TCCAGAACTG	CTGAAGAGA	ACTGCTTGGA	ATTATGGGAA	4500
GGCAGTTCAT	TGTTACTGTA	ACTGATTGTA	TTATTKKGTG	AAATATTTCT	ATAAATATTT	4560
AARAGGTGTA	CACATGTAAT	ATACATGGAA	ATGCTGTACA	GTCTATTTCC	TGGGGCCTCT	4620
CCACTCCTGC	CCCAGAGTGG	GGAGACCACA	GGGGCCCTTT	CCCCTGTGTA	CATTGGTCTC	4680
TGTGCCACAA	CCAAGCTTAA	CTTAGTTTTA	AAAAAAATCT	CCCAGCATAT	GTCGCTGCTG	4740

CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800
TATTTGTAAA GGTTTCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860
ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920
ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980
GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040
TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100
GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160
CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Ala	Pro	Asp	Ser	Glu	Ala	Pro	Ser	Asn	Pro	Arg	Ile	Thr	Ala	1	5	10	15
Ala	His	Glu	Ser	Pro	Cys	Ala	Thr	Glu	Ala	Arg	His	Ser	Ala	Asp	Leu	20	25	30	
Tyr	Ile	Arg	Thr	Ser	Trp	Val	Asp	Ala	Ala	Leu	Ala	Leu	Ser	Glu	Leu	35	40	45	
Glu	Lys	Gly	Asn	Ile	Glu	Gly	Gly	Arg	Thr	Ser	Leu	Trp	Ile	Arg	Ala	50	55	60	
Trp	Leu	Gln	Glu	Gln	Leu	Phe	Ile	Leu	Gly	Cys	Phe	Leu	Gln	Gly	Asp	65	70	75	80
Ala	Gly	Lys	Val	Leu	Phe	Val	Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	85	90	95	
Val	Gly	Leu	Lys	Ser	Ala	Gln	Ile	His	Thr	Arg	Val	Asp	Gln	Leu	Trp	100	105	110	
Val	Gln	Glu	Gly	Gly	Arg	Leu	Glu	Ala	Glu	Leu	Lys	Tyr	Thr	Ala	Gln	115	120	125	
Ala	Leu	Gly	Glu	Ala	Asp	Ser	Ser	Thr	His	Gln	Leu	Val	Ile	Gln	Thr	130	135	140	

09754032.016301

Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu
145 150 155 160

His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr
165 170 175

Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro
180 185 190

Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile
195 200 205

Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys
210 215 220

Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys
225 230 235 240

Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys
245 250 255

Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys
260 265 270

Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro
275 280 285

Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His
290 295 300

Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala
305 310 315 320

Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr
325 330 335

Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val
340 345 350

Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His
355 360 365

Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val
370 375 380

Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr
385 390 395 400

Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr
405 410 415

Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys
420 425 430

Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr
435 440 445

Leu Ile Gln Trp Arg Asp Pro Ile Arg Ser Gln Ala Gly Val Gly Ile

0954033 010301

450	455	460
Ala Gly Val Leu Leu Leu Ser Ile Thr Val	Ala Ala Gly Leu Gly Phe	
465	470	475 480
Cys Ala Leu Leu Gly Ile Pro Phe Asn	Ala Ser Ser Thr Gln Ile Val	
	485 490 495	
Pro Phe Leu Ala Leu Gly Leu Gly Val Gln Asp Met Phe Leu Leu Thr		
	500 505 510	
His Thr Tyr Val Glu Gln Ala Gly Asp Val Pro Arg Glu Glu Arg Thr		
	515 520 525	
Gly Leu Val Leu Lys Lys Ser Gly Leu Ser Val Leu Leu Ala Ser Leu		
	530 535 540	
Cys Asn Val Met Ala Phe Leu Ala Ala Ala Leu Leu Pro Ile Pro Ala		
	545 550 555 560	
Phe Arg Val Phe Cys Leu Gln Ala Ala Ile Leu Leu Leu Phe Asn Leu		
	565 570 575	
Gly Ser Ile Leu Leu Val Phe Pro Ala Met Ile Ser Leu Asp Leu Arg		
	580 585 590	
Arg Arg Ser Ala Ala Arg Ala Asp Leu Leu Cys Cys Leu Met Pro Glu		
	595 600 605	
Ser Pro Leu Pro Lys Lys Lys Ile Pro Glu Arg Ala Lys Thr Arg Lys		
	610 615 620	
Asn Asp Lys Thr His Arg Ile Asp Thr Thr Arg Gln Pro Leu Asp Pro		
	625 630 635 640	
Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu		
	645 650 655	
Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala		
	660 665 670	
Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser		
	675 680 685	
Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile		
	690 695 700	
Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys		
	705 710 715 720	
Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu		
	725 730 735	
Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val		
	740 745 750	
Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe		
	755 760 765	

00784032 010304

Trp	Leu	Ser	Leu	Phe	Arg	Asp	Trp	Leu	Leu	Asp	Leu	Gln	Val	Ala	Phe		
770						775					780						
Asp	Lys	Glu	Val	Ala	Ser	Gly	Cys	Ile	Thr	Gln	Glu	Tyr	Trp	Cys	Lys		
785					790					795					800		
Asn	Ala	Ser	Asp	Glu	Gly	Ile	Leu	Ala	Tyr	Lys	Leu	Met	Val	Gln	Thr		
				805					810					815			
Gly	His	Val	Asp	Asn	Pro	Ile	Asp	Lys	Ser	Leu	Ile	Thr	Ala	Gly	His		
			820					825						830			
Arg	Leu	Val	Asp	Lys	Asp	Gly	Ile	Ile	Asn	Pro	Lys	Ala	Phe	Tyr	Asn		
		835					840						845				
Tyr	Leu	Ser	Ala	Trp	Ala	Thr	Asn	Asp	Ala	Leu	Ala	Tyr	Gly	Ala	Ser		
	850					855					860						
Gln	Gly	Asn	Leu	Lys	Pro	Gln	Pro	Gln	Arg	Trp	Ile	His	Ser	Pro	Glu		
865					870					875					880		
Asp	Val	His	Leu	Glu	Ile	Lys	Lys	Ser	Ser	Pro	Leu	Ile	Tyr	Thr	Gln		
				885					890						895		
Leu	Pro	Phe	Tyr	Leu	Ser	Gly	Leu	Ser	Asp	Thr	Xaa	Ser	Ile	Lys	Thr		
			900					905						910			
Leu	Ile	Arg	Ser	Val	Arg	Asp	Leu	Cys	Leu	Lys	Tyr	Glu	Ala	Lys	Gly		
	915						920						925				
Leu	Pro	Asn	Phe	Pro	Ser	Gly	Ile	Pro	Phe	Leu	Phe	Trp	Glu	Gln	Tyr		
	930					935						940					
Leu	Tyr	Leu	Arg	Thr	Ser	Leu	Leu	Leu	Ala	Leu	Ala	Cys	Ala	Leu	Ala		
945					950					955					960		
Ala	Val	Phe	Ile	Ala	Val	Met	Val	Leu	Leu	Leu	Asn	Ala	Trp	Ala	Ala		
				965					970						975		
Val	Leu	Val	Thr	Leu	Ala	Leu	Ala	Thr	Leu	Val	Leu	Gln	Leu	Leu	Gly		
			980					985						990			
Val	Met	Ala	Leu	Leu	Gly	Val	Lys	Leu	Ser	Ala	Met	Pro	Ala	Val	Leu		
	995						1000						1005				
Leu	Val	Leu	Ala	Ile	Gly	Arg	Gly	Val	His	Phe	Thr	Val	His	Leu	Cys		
	1010					1015						1020					
Leu	Gly	Phe	Val	Thr	Ser	Ile	Gly	Cys	Lys	Arg	Arg	Arg	Ala	Ser	Leu		
1025					1030					1035					1040		
Ala	Leu	Glu	Ser	Val	Leu	Ala	Pro	Val	Val	His	Gly	Ala	Leu	Ala	Ala		
				1045					1050						1055		
Ala	Leu	Ala	Ala	Ser	Met	Leu	Ala	Ala	Ser	Glu	Cys	Gly	Phe	Val	Ala		
		1060						1065						1070			
Arg	Leu	Phe	Leu	Arg	Leu	Leu	Leu	Asp	Ile	Val	Phe	Leu	Gly	Leu	Ile		

1075	1080	1085
Asp Gly Leu Leu Phe Phe Pro Ile Val Leu Ser Ile Leu Gly Pro Ala 1090	1095	1100
Ala Glu Val Arg Pro Ile Glu His Pro Glu Arg Leu Ser Thr Pro Ser 1105	1110	1115 1120
Pro Lys Cys Ser Pro Ile His Pro Arg Lys Ser Ser Ser Ser Ser Gly 1125	1130	1135
Gly Gly Asp Lys Ser Ser Arg Thr Ser Lys Ser Ala Pro Arg Pro Cys 1140	1145	1150
Ala Pro Ser Leu Thr Thr Ile Thr Glu Glu Pro Ser Ser Trp His Ser 1155	1160	1165
Ser Ala His Ser Val Gln Ser Ser Met Gln Ser Ile Val Val Gln Pro 1170	1175	1180
Glu Val Val Val Glu Thr Thr Thr Tyr Asn Gly Ser Asp Ser Ala Ser 1185	1190	1195 1200
Gly Arg Ser Thr Pro Thr Lys Ser Ser His Gly Gly Ala Ile Thr Thr 1205	1210	1215
Thr Lys Val Thr Ala Thr Ala Asn Ile Lys Val Glu Val Val Thr Pro 1220	1225	1230
Ser Asp Arg Lys Ser Arg Arg Ser Tyr His Tyr Tyr Asp Arg Arg Arg 1235	1240	1245
Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg 1250	1255	1260
Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg 1265	1270	1275 1280
Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg 1285	1290	1295
Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr 1300	1305	1310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTCGCCC	60
ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCCGCTG GGCAAGAGAG AGTGAGAGAG	120
AGAAACAGCG GCGCGCGCTC GCCTAATGAA GTTGTGGCC TGGCTGGCGT GCCGCATCCA	180
CGAGATACAG ATACATCTCT CATGGACCGC GACAGCCTCC CACGCGTTCC GGACACACAC	240
GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTTACA TACGCACCAG CTGGGTGGAC	300
GCCCAAGTGG CGCTCGATCA GATAGATAAG GGCAAGCGC GTGGCAGCCG CACGGCGATC	360
TATCTGCGAT CAGTATTCCA GTCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAGCAC	420
GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG	480
AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG	540
GCGGAACTGG CCTACACACA GAAGACGATC GCGGAGGACG AGTCGGCCAC GCATCAGCTG	600
CTCATTCAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC ATCCGCAGGC GCTGCTTGCC	660
CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG	720
GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTACTACATC	780
GAGCAGATCC TCGGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTTCTGG	840
GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA	900
CTCCTGTGGA CCACCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC	960
GAGGAAAAGA TCAGCTTCGA CTTTCGAGACC GTGGAGCAGT ACATGAAGCG TCGGGCCATT	1020
GGCAGTGGCT ACATGGAGAA GCCCTGCCTG AACCCACTGA ATCCCAATTG CCCGGACACG	1080
GCACCGAACA AGAACAGCAC CCAGCCGCCG GATGTGGGAG CCATCCTGTC CGGAGGCTGC	1140
TACGGTTATG CCGCGAAGCA CATGCACTGG CCGGAGGAGC TGATTGTGGG CGGACGGAAG	1200
AGGAACCGCA GCGGACACTT GAGGAAGGCC CAGGCCCTGC AGTCGGTGGT GCAGCTGATG	1260
ACCGAGAAGG AAATGTACGA CCAGTGGCAG GACAACTACA AGGTGCACCA TCTTGGATGG	1320
ACGCAGGAGA AGGCAGCGGA GGTTTTGAAC GCCTGGCAGC GCAACTTTTC GCGGGAGGTG	1380
GAACAGCTGC TACGTAAACA GTCGAGAATT GCCACCAACT ACGATATCTA CGTGTTACGC	1440
TCGGCTGCAC TGGATGACAT CCTGGCCAAG TTCTCCCATC CCAGCGCCTT GTCCATTGTC	1500
ATCGGCGTGG CCGTCACCGT TTTGTATGCC TTTTGCACGC TCCTCCGCTG GAGGGACCCC	1560
GTCCGTGGCC AGAGCAGTGT GGGCGTGGCC GGAGTTCTGC TCATGTGCTT CAGTACCGCC	1620
GCCGATTGG GATTGTCAGC CCTGCTCGGT ATCGTTTTCA ATGCGCTGAC CGCTGCCTAT	1680
GCGGAGAGCA ATCGGCGGGA GCAGACCAAG CTGATTCTCA AGAACGCCAG CACCCAGGTG	1740

GTTCCGTTTT	TGGCCCTTGG	TCTGGGCGTC	GATCACATCT	TCATAGTGGG	ACCGAGCATC	1800
CTGTTTCAGTG	CCTGCAGCAC	CGCAGGATCC	TTCTTTGCGG	CCGCCTTTAT	TCCGGTGCCG	1860
GCTTTGAAGG	TATTCTGTCT	GCAGGCTGCC	ATCGTAATGT	GCTCCAATTT	GGCAGCGGCT	1920
CTATTGGTTT	TTCCGGCCAT	GATTTCTGTTG	GATCTACGGA	GACGTACCGC	CGGCAGGGCG	1980
GACATCTTCT	GCTGCTGTTT	TCCGGTGTGG	AAGGAACAGC	CGAAGGTGGC	ACCTCCGGTG	2040
CTGCCGCTGA	ACAACAACAA	CGGGCGCGGG	GCCCGGCATC	CGAAGAGCTG	CAACAACAAC	2100
AGGGTGCCGC	TGCCCCCCCA	GAATCCTCTG	CTGGAACAGA	GGGCAGACAT	CCCTGGGAGC	2160
AGTCACTCAC	TGGCGTCCTT	CTCCCTGGCA	ACCTTCGCCT	TTCAGCACTA	CACTCCCTTC	2220
CTCATGCGCA	GCTGGGTGAA	GTTCTTGACC	GTTATGGGTT	TCCTGGCGGC	CCTCATATCC	2280
AGCTTGATATG	CCTCCACGCG	CCTTCAGGAT	GGCCTGGACA	TTATTGATCT	GGTGCCCAAG	2340
GACAGCAACG	AGCACAAAGT	CCTGGATGCT	CAAACCTCGGC	TCTTTGGCTT	CTACAGCATG	2400
TATGCGGTTA	CCCAGGGCAA	CTTTGAATAT	CCCACCCAGC	AGCAGTTGCT	CAGGGACTAC	2460
CATGATTCTT	TTGTGCGGGT	GCCACATGTG	ATCAAGAATG	ATAACGGTGG	ACTGCCGGAC	2520
TTCTGGCTGC	TGCTCTTCAG	CGAGTGGCTG	GGTAATCTGC	AAAAGATATT	CGACGAGGAA	2580
TACCGCGACG	GACGGCTGAC	CAAGGAGTGC	TGGTTCCCAA	ACGCCAGCAG	CGATGCCATC	2640
CTGGCCTACA	AGCTAATCGT	GCAAACCGGC	CATGTGGACA	ACCCCGTGGA	CAAGGAAGTG	2700
GTGCTCACCA	ATCGCCTGGT	CAACAGCGAT	GGCATCATCA	ACCAACGCGC	CTTCTACAAC	2760
TATCTGTTCG	CATGGGCCAC	CAACGACGTC	TTGCCTACG	GAGCTTCTCA	GGGCAAATTG	2820
TATCCGGAAC	CGCGCCAGTA	TTTTACACAA	CCCAACGAGT	ACGATCTTAA	GATACCCAAG	2880
AGTCTGCCAT	TGGTCTACGC	TCAGATGCCC	TTTACCTCC	ACGGACTAAC	AGATACCTCG	2940
CAGATCAAGA	CCCTGATAGG	TCATATTCGC	GACCTGAGCG	TCAAGTACGA	GGGCTTCGGC	3000
CTGCCCAACT	ATCCATCGGG	CATTCCCTTC	ATCTTCTGGG	AGCAGTACAT	GACCCTGCGC	3060
TCCTCACTGG	CCATGATCCT	GGCCTGCGTG	CTACTCGCCG	CCCTGGTGCT	GGTCTCCCTG	3120
CTCCTGCTCT	CCGTTTGGGC	CGCCGTTCTC	GTGATCCTCA	GCGTTCTGGC	CTCGCTGGCC	3180
CAGATCTTTG	GGGCCATGAC	TCTGCTGGGC	ATCAAACCTCT	CGGCCATTCC	GGCAGTCATA	3240
CTCATCCTCA	GCGTGGGCAT	GATGCTGTGC	TTCAATGTGC	TGATATCACT	GGGCTTCATG	3300
ACATCCGTTG	GCAACCGACA	GCGCCGCGTC	CAGCTGAGCA	TGCAGATGTC	CCTGGGACCA	3360
CTTGTCACG	GATGCTGAC	CTCCGGAGTG	GCCGTGTTCA	TGCTCTCCAC	GTCGCCCTTT	3420
GAGTTTGTGA	TCCGGCACTT	CTGCTGGCTT	CTGCTGGTGG	TCTTATGCGT	TGGCGCCTGC	3480

Thr	Leu	Gly	Ser	Ser	Val	Gln	Lys	His	Ala	Gly	Lys	Val	Leu	Phe	Val		65	70	75	80
Ala	Ile	Leu	Val	Leu	Ser	Thr	Phe	Cys	Val	Gly	Leu	Lys	Ser	Ala	Gln		85	90	95	
Ile	His	Ser	Lys	Val	His	Gln	Leu	Trp	Ile	Gln	Glu	Gly	Gly	Arg	Leu		100	105	110	
Glu	Ala	Glu	Leu	Ala	Tyr	Thr	Gln	Lys	Thr	Ile	Gly	Glu	Asp	Glu	Ser		115	120	125	
Ala	Thr	His	Gln	Leu	Leu	Ile	Gln	Thr	Thr	His	Asp	Pro	Asn	Ala	Ser		130	135	140	
Val	Leu	His	Pro	Gln	Ala	Leu	Leu	Ala	His	Leu	Glu	Val	Leu	Val	Lys		145	150	155	160
Ala	Thr	Ala	Val	Lys	Val	His	Leu	Tyr	Asp	Thr	Glu	Trp	Gly	Leu	Arg		165	170	175	
Asp	Met	Cys	Asn	Met	Pro	Ser	Thr	Pro	Ser	Phe	Glu	Gly	Ile	Tyr	Tyr		180	185	190	
Ile	Glu	Gln	Ile	Leu	Arg	His	Leu	Ile	Pro	Cys	Ser	Ile	Ile	Thr	Pro		195	200	205	
Leu	Asp	Cys	Phe	Trp	Glu	Gly	Ser	Gln	Leu	Leu	Gly	Pro	Glu	Ser	Ala		210	215	220	
Val	Val	Ile	Pro	Gly	Leu	Asn	Gln	Arg	Leu	Leu	Trp	Thr	Thr	Leu	Asn		225	230	235	240
Pro	Ala	Ser	Val	Met	Gln	Tyr	Met	Lys	Gln	Lys	Met	Ser	Glu	Glu	Lys		245	250	255	
Ile	Ser	Phe	Asp	Phe	Glu	Thr	Val	Glu	Gln	Tyr	Met	Lys	Arg	Ala	Ala		260	265	270	
Ile	Gly	Ser	Gly	Tyr	Met	Glu	Lys	Pro	Cys	Leu	Asn	Pro	Leu	Asn	Pro		275	280	285	
Asn	Cys	Pro	Asp	Thr	Ala	Pro	Asn	Lys	Asn	Ser	Thr	Gln	Pro	Pro	Asp		290	295	300	
Val	Gly	Ala	Ile	Leu	Ser	Gly	Gly	Cys	Tyr	Gly	Tyr	Ala	Ala	Lys	His		305	310	315	320
Met	His	Trp	Pro	Glu	Glu	Leu	Ile	Val	Gly	Gly	Arg	Lys	Arg	Asn	Arg		325	330	335	
Ser	Gly	His	Leu	Arg	Lys	Ala	Gln	Ala	Leu	Gln	Ser	Val	Val	Gln	Leu		340	345	350	
Met	Thr	Glu	Lys	Glu	Met	Tyr	Asp	Gln	Trp	Gln	Asp	Asn	Tyr	Lys	Val		355	360	365	
His	His	Leu	Gly	Trp	Thr	Gln	Glu	Lys	Ala	Ala	Glu	Val	Leu	Asn	Ala					

370					375					380					
Trp	Gln	Arg	Asn	Phe	Ser	Arg	Glu	Val	Glu	Gln	Leu	Leu	Arg	Lys	Gln
385					390					395					400
Ser	Arg	Ile	Ala	Thr	Asn	Tyr	Asp	Ile	Tyr	Val	Phe	Ser	Ser	Ala	Ala
				405					410					415	
Leu	Asp	Asp	Ile	Leu	Ala	Lys	Phe	Ser	His	Pro	Ser	Ala	Leu	Ser	Ile
			420						425					430	
Val	Ile	Gly	Val	Ala	Val	Thr	Val	Leu	Tyr	Ala	Phe	Cys	Thr	Leu	Leu
		435							440					445	
Arg	Trp	Arg	Asp	Pro	Val	Arg	Gly	Gln	Ser	Ser	Val	Gly	Val	Ala	Gly
									455					460	
Val	Leu	Leu	Met	Cys	Phe	Ser	Thr	Ala	Ala	Gly	Leu	Gly	Leu	Ser	Ala
465					470					475					480
Leu	Leu	Gly	Ile	Val	Phe	Asn	Ala	Leu	Thr	Ala	Ala	Tyr	Ala	Glu	Ser
				485					490					495	
Asn	Arg	Arg	Glu	Gln	Thr	Lys	Leu	Ile	Leu	Lys	Asn	Ala	Ser	Thr	Gln
			500						505					510	
Val	Val	Pro	Phe	Leu	Ala	Leu	Gly	Leu	Gly	Val	Asp	His	Ile	Phe	Ile
			515						520					525	
Val	Gly	Pro	Ser	Ile	Leu	Phe	Ser	Ala	Cys	Ser	Thr	Ala	Gly	Ser	Phe
	530								535					540	
Phe	Ala	Ala	Ala	Phe	Ile	Pro	Val	Pro	Ala	Leu	Lys	Val	Phe	Cys	Leu
545					550					555					560
Gln	Ala	Ala	Ile	Val	Met	Cys	Ser	Asn	Leu	Ala	Ala	Ala	Leu	Leu	Val
				565					570					575	
Phe	Pro	Ala	Met	Ile	Ser	Leu	Asp	Leu	Arg	Arg	Arg	Thr	Ala	Gly	Arg
			580						585					590	
Ala	Asp	Ile	Phe	Cys	Cys	Cys	Phe	Pro	Val	Trp	Lys	Glu	Gln	Pro	Lys
			595						600					605	
Val	Ala	Pro	Pro	Val	Leu	Pro	Leu	Asn	Asn	Asn	Asn	Gly	Arg	Gly	Ala
				610					615					620	
Arg	His	Pro	Lys	Ser	Cys	Asn	Asn	Asn	Arg	Val	Pro	Leu	Pro	Ala	Gln
625					630					635					640
Asn	Pro	Leu	Leu	Glu	Gln	Arg	Ala	Asp	Ile	Pro	Gly	Ser	Ser	His	Ser
				645					650					655	
Leu	Ala	Ser	Phe	Ser	Leu	Ala	Thr	Phe	Ala	Phe	Gln	His	Tyr	Thr	Pro
			660						665					670	
Phe	Leu	Met	Arg	Ser	Trp	Val	Lys	Phe	Leu	Thr	Val	Met	Gly	Phe	Leu
			675						680					685	

Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly
 690 695 700
 Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe
 705 710 715 720
 Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val
 725 730 735
 Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp
 740 745 750
 Tyr His Asp Ser Phe Arg Val Pro His Val Ile Lys Asn Asp Asn Gly
 755 760 765
 Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly Asn
 770 775 780
 Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr Lys
 785 790 795 800
 Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr Lys
 805 810 815
 Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu Leu
 820 825 830
 Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln Arg
 835 840 845
 Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe Ala
 850 855 860
 Tyr Gly Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr Phe
 865 870 875 880
 His Gln Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro Leu
 885 890 895
 Val Tyr Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr Ser
 900 905 910
 Gln Ile Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys Tyr
 915 920 925
 Glu Gly Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile Phe
 930 935 940
 Trp Glu Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu Ala
 945 950 955 960
 Cys Val Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu Leu Ser
 965 970 975
 Val Trp Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu Ala
 980 985 990
 Gln Ile Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala Ile

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995	1000	1005
Pro Ala Val Ile Leu Ile Leu Ser Val Gly Met Met Leu Cys Phe Asn 1010 1015 1020		
Val Leu Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln Arg 1025 1030 1035 1040		
Arg Val Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His Gly 1045 1050 1055		
Met Leu Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro Phe 1060 1065 1070		
Glu Phe Val Ile Arg His Phe Cys Trp Leu Leu Leu Val Val Leu Cys 1075 1080 1085		
Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser Met 1090 1095 1100		
Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg Ile 1105 1110 1115 1120		
Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly Lys 1125 1130 1135		
Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln Lys 1140 1145 1150		
Ser His His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr Thr 1155 1160 1165		
Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile Gln 1170 1175 1180		
Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala Ser 1185 1190 1195 1200		
Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln His 1205 1210 1215		
His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro Thr 1220 1225 1230		
Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val Thr 1235 1240 1245		
Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala Thr 1250 1255 1260		
Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg Ser 1265 1270 1275 1280		
Tyr Asn Phe Thr Ser 1285		

(2) INFORMATION FOR SEQ ID NO:7:

項目	単位	値
総人口	人	1,234,567
男性人口	人	612,345
女性人口	人	622,222
人口密度	人/平方キロメートル	123.4
出生率	‰	10.5
死亡率	‰	8.2
自然増減率	‰	2.3
平均寿命	歳	75.8
識字率	%	98.5
労働力人口	人	567,890
失業率	%	5.2
産業別人口	人	
農業	人	123,456
工業	人	234,567
商業	人	145,678
サービス業	人	364,189
所得総額	億円	1,234,567
一人当たり所得	円	1,234,567
財政収支	億円	
歳入	億円	123,456
歳出	億円	134,567
収支差	億円	-11,111
外債残高	億円	567,890
貿易収支	億円	
輸出	億円	123,456
輸入	億円	134,567
収支差	億円	-11,111
対外貿易依存度	%	15.2
対外貿易のGDPに対する割合	%	25.8
対外貿易の人口に対する割合	%	1.2
対外貿易の労働力に対する割合	%	0.8
対外貿易の所得に対する割合	%	0.5
対外貿易の財政収支に対する割合	%	0.3
対外貿易の貿易収支に対する割合	%	0.2
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収支に対する割合	%	0.1
対外貿易の輸出に対する割合	%	0.1
対外貿易の輸入に対する割合	%	0.1
対外貿易の収支差に対する割合	%	0.1
対外貿易の外債残高に対する割合	%	0.1
対外貿易の貿易収		

- (ii) MOLECULE TYPE: DNA (genomic)

AAGGTCCATC	AGCTTTGGAT	ACAGGAAGGT	GGTTCGCTCG	AGCATGAGCT	AGCCTACACG	60
CAGAAATCGC	TCGGCGAGAT	GGACTCCTCC	ACGCACCAGC	TGCTAATCCA	AACNCCCAA	120
GATATGGACG	CCTCGATACT	GCACCCGAAC	GCGCTACTGA	CGCACCTGGA	CGTGGTGAAG	180
AAAGCGATCT	CGGTGACGGT	GCACATGTAC	GACATCACGT	GGAGNCTCAA	GGACATGTGC	240
TACTCGCCCA	GCATACCGAG	NTTCGATACG	CACTTTATCG	AGCAGATCTT	CGAGAACATC	300
ATACCGTGCG	CGATCATCAC	GCCGCTGGAT	TGCTTTTGGG	AGGGA		345

(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

42

Phe Glu Asn Ile Ile Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe
100 105 110

Trp Glu Gly
115

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC	60
CCAGGCGCGC CCGGAGCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC	120
GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC	180
GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG	240
GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG	300
TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAA AGAACTGCGG CAAGTTTTTG	360
GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG	420
ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT	480
ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA	540
AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGA CTCAGCA	600
CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG	660
TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC	720
CTTTACCCTT GCTTAATCAT TACACCTTG GACTGCTTCT GGGAAGGGGC AAAGCTACAG	780
TCCGGGACAG CATACTCCT AGGTAAGCCT COTTTACGGT GGACAACTT TGACCCCTTG	840
GAATTCCTAG AAGAGTTAAA GAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG	900
AATAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA	960
GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT	1020
TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT	1080
GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAAGTTGTCA GCGCTCACGC CCTGCAAACC	1140

ATGTTCCAGT	TAATGACTCC	CAAGCAAATG	TATGAACACT	TCAGGGGCTA	CGACTATGTC	1200
TCTCACATCA	ACTGGAATGA	AGACAGGGCA	GCCGCCATCC	TGGAGGCCTG	GCAGAGGACT	1260
TACGTGGAGG	TGGTTCATCA	AAGTGTGCGC	CCAAACTCCA	CTCAAAGGT	GCTTCCCTTC	1320
ACAACCACGA	CCCTGGACGA	CATCCTAAAA	TCCTTCTCTG	ATGTCAGTGT	CATCCGAGTG	1380
GCCAGCGGCT	ACCTACTGAT	GCTTGCCTAT	GCCTGTTTAA	CCATGCTGCG	CTGGGACTGC	1440
TCCAAGTCCC	AGGGTGCCGT	GGGGCTGGCT	GGCGTCCTGT	TGGTTGCGCT	GTCAGTGGCT	1500
GCAGGATTGG	GCCTCTGCTC	CTTGATTGGC	ATTTCTTTTA	ATGCTGCGAC	AACTCAGGTT	1560
TTGCCGTTTC	TTGCTCTTGG	TGTTGGTGTG	GATGATGTCT	TCCTCCTGGC	CCATGCATTTC	1620
AGTGAAACAG	GACAGAATAA	GAGGATTCCA	TTTGAGGACA	GGACTGGGGA	GTGCCTCAAG	1680
CGCACCGGAG	CCAGCGTGCC	CCTCACCTCC	ATCAGCAATG	TCACCGCCTT	CTTCATGGCC	1740
GCATTGATCC	CTATCCCTGC	CCTGCGAGCG	TTCTCCCTCC	AGGCTGCTGT	GGTGGTGGTA	1800
TTCAATTTTG	CTATGGTTCT	GCTCATTTTT	CCTGCAATTC	TCAGCATGGA	TTTATACAGA	1860
CGTGAGGACA	GAAGATTGGA	TATTTTCTGC	TGTTTCACAA	GCCCCTGTGT	CAGCAGGGTG	1920
ATTCAAGTTG	AGCCACAGGC	CTACACAGAG	CCTCACAGTA	ACACCCGGTA	CAGCCCCCCA	1980
CCCCCATACA	CCAGCCACAG	CTTCGCCAC	GAAACCCATA	TCACTATGCA	GTCCACCGTT	2040
CAGCTCCGCA	CAGAGTATGA	CCCTCACACG	CACGTGTACT	ACACCACCGC	CGAGCCACGC	2100
TCTGAGATCT	CTGTACAGCC	TGTTACCGTC	ACCCAGGACA	ACCTCAGCTG	TCAGAGTCCC	2160
GAGAGCACCA	GCTCTACCAG	GGACCTGCTC	TCCCAGTTCT	CAGACTCCAG	CCTCCACTGC	2220
CTCGAGCCCC	CCTGCACCAA	GTGGACACTC	TCTTCGTTTG	CAGAGAAGCA	CTATGCTCCT	2280
TTCCTCCTGA	AACCCAAAGC	CAAGGTTGTG	GTAATCCTTC	TTTTCCTGGG	CTTGCTGGGG	2340
GTCAGCCTTT	ATGGGACCAC	CCGAGTGAGA	GACGGGCTGG	ACCTCACGGA	CATTGTTCCC	2400
CGGGAAACCA	GAGAATATGA	CTTCATAGCT	GCCCAGTTCA	AGTACTTCTC	TTTCTACAAC	2460
ATGTATATAG	TCACCCAGAA	AGCAGACTAC	CCGAATATCC	AGCACCTACT	TTACGACCTT	2520
CATAAGAGTT	TCAGCAATGT	GAAGTATGTC	ATGCTGGAGG	AGAACAAGCA	ACTTCCCCAA	2580
ATGTGGCTGC	ACTACTTTAG	AGACTGGCTT	CAAGGACTTC	AGGATGCATT	TGACAGTGAC	2640
TGGGAAACTG	GGAGGATCAT	GCCAAACAAT	TATAAAAATG	GATCAGATGA	CGGGGTCCTC	2700
GCTTACAAAC	TCCTGGTGCA	GA CTGGCAGC	CGAGACAAGC	CCATCGACAT	TAGTCAGTTG	2760
ACTAAACAGC	GTCTGGTAGA	CGCAGATGGC	ATCATTAATC	CGAGCGCTTT	CTACATCTAC	2820
CTGACCGCTT	GGGT CAGCAA	CGACCCTGTA	GCTTACGCTG	CCTCCCAGGC	CAACATCCGG	2880

CCTCACCGGC	CGGAGTGGGT	CCATGACAAA	GCCGACTACA	TGCCAGAGAC	CAGGCTGAGA	2940
ATCCCAGCAG	CAGAGCCCAT	CGAGTACGCT	CAGTTCCCTT	TCTACCTCAA	CGGCCTACGA	3000
GACACCTCAG	ACTTTGTGGA	AGCCATAGAA	AAAGTGAGAG	TCATCTGTAA	CAACTATACG	3060
AGCCTGGGAC	TGTCCAGCTA	CCCCAATGGC	TACCCCTTCC	TGTTCTGGGA	GCAATACATC	3120
AGCCTGCGCC	ACTGGCTGCT	GCTATCCATC	AGCGTGGTGC	TGGCCTGCAC	GTTTCTAGTG	3180
TGCGCAGTCT	TCCTCCTGAA	CCCCTGGACG	GCCGGGATCA	TTGTCATGGT	CCTGGCTCTG	3240
ATGACCGTTG	AGCTCTTTGG	CATGATGGGC	CTCATTGGGA	TCAAGCTGAG	TGCTGTGCCT	3300
GTGGTCATCC	TGATTGCATC	TGTTGGCATC	GGAGTGGAGT	TCACCGTCCA	CGTGGCTTTG	3360
GCCTTTCTGA	CAGCCATTGG	GGACAAGAAC	CACAGGGCTA	TGCTCGCTCT	GGAACACATG	3420
TTTGCTCCCG	TTCTGGACGG	TGCTGTGTCC	ACTCTGCTGG	GTGTACTGAT	GCTTGCAGGG	3480
TCCGAATTTG	ATTTTCATTGT	CAGATACTTC	TTTGCCGTCC	TGGCCATTCT	CACCGTCTTG	3540
GGGGTTCTCA	ATGGACTGGT	TCTGCTGCCT	GTCTCTTAT	CCTTCTTTGG	ACCGTGTCTT	3600
GAGGTGTCTC	CAGCCAATGG	CCTAAACCGA	CTGCCCACTC	CTTCGCCTGA	GCCGCCTCCA	3660
AGTGTCGTCC	GGTTTGCCGT	GCCTCCTGGT	CACACGAACA	ATGGGTCTGA	TTCTCCGAC	3720
TCGGAGTACA	GCTCTCAGAC	CACGGTGTCT	GGCATCAGTG	AGGAGCTCAG	GCAATACGAA	3780
GCACAGCAGG	GTGCCGGAGG	CCCTGCCCCAC	CAAGTGATTG	TGGAAGCCAC	AGAAAACCTT	3840
GTCTTTGCCC	GGTCCACTGT	GGTCCATCCG	GACTCCAGAC	ATCAGCCTCC	CTTGACCCCT	3900
CGGCAACAGC	CCCACCTGGA	CTCTGGCTCC	TTGTCCCCTG	GACGGCAAGG	CCAGCAGCCT	3960
CGAAGGGATC	CCCCTAGAGA	AGGCTTGCGG	CCACCCCCCT	ACAGACCGCG	CAGAGACGCT	4020
TTTGAAATTT	CTACTGAAGG	GCATTCTGGC	CCTAGCAATA	GGGACCGCTC	AGGGCCCCGT	4080
GGGGCCCGTT	CTCACAACCC	TCGGAACCCA	ACGTCCACCG	CCATGGGCAG	CTCTGTGCCC	4140
AGCTACTGCC	AGCCCATCAC	CACTGTGACG	GCTTCTGCTT	CGGTGACTGT	TGCTGTGCAT	4200
CCCCCGCCTG	GACCTGGGCG	CAACCCCCGA	GGGGGGCCCT	GTCCAGGCTA	TGAGAGCTAC	4260
CCTGAGACTG	ATCACGGGGT	ATTTGAGGAT	CCTCATGTGC	CTTTTCATGT	CAGGTGTGAG	4320
AGGAGGGACT	CAAAGGTGGA	GGTCATAGAG	CTACAGGACG	TGGAATGTGA	GGAGAGGCCG	4380
TGGGGGAGCA	GCTCCAACCTG	AGGGTAATTA	AAATCTGAAG	CAAAGAGGCC	AAAGATTGGA	4440
AAGCCCCGCC	CCCACCTCTT	TCCAGAAGCTG	CTTGAAGAGA	ACTGCTTGGA	ATTATGGGAA	4500
GGCAGTTCAT	TGTTACTGTA	ACTGATTGTA	TTATTKKGTG	AAATATTTCT	ATAAATATTT	4560
AARAGGTGTA	CACATGTAAT	ATACATGGAA	ATGCTGTACA	GTCTATTTCC	TGGGGCCTCT	4620

CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680
TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAATCT CCCAGCATAT GTCGCTGCTG 4740
CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800
TATTTGTAAA GGTTCCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860
ATGAATTGTT ACTGTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920
ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980
GGTGGATGTG TGTGTGCATG TGA CTTTCCA ATG TACTGTA TTGTGGTTTG TTGTTGTTGT 5040
TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100
GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160
CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1434 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Ala Gly Asn Ala Ala Gly Ala Leu Gly Arg Gln Ala Gly
1 5 10 15
Gly Gly Arg Arg Arg Arg Thr Gly Gly Pro His Arg Ala Ala Pro Asp
20 25 30
Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu
35 40 45
Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp
50 55 60
Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile
65 70 75 80
Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly
85 90 95
Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu
100 105 110
Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr
115 120 125

Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met	130	135	140
Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala	145	150	155 160
Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val	165	170	175
Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser	180	185	190
Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr	195	200	205
Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly	210	215	220
Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu	225	230	235 240
Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys	245	250	255
Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu	260	265	270
Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro	275	280	285
Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp	290	295	300
Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr	305	310	315 320
Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala	325	330	335
Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu	340	345	350
Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val	355	360	365
Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala	370	375	380
Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn	385	390	395 400
Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile	405	410	415
Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr	420	425	430
Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys			

435	440	445
Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala 450 455 460		
Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser 465 470 475 480		
Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val 485 490 495		
Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly 500 505 510		
Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys 515 520 525		
Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala 530 535 540		
Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser 545 550 555 560		
Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu 565 570 575		
Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg 580 585 590		
Arg Leu Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val 595 600 605		
Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg 610 615 620		
Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr 625 630 635 640		
His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro 645 650 655		
His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser 660 665 670		
Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro 675 680 685		
Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser 690 695 700		
Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser 705 710 715 720		
Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys 725 730 735		
Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr 740 745 750		

Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro
755 760 765

Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe
770 775 780

Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn
785 790 795 800

Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys
805 810 815

Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His
820 825 830

Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp
835 840 845

Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp
850 855 860

Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp
865 870 875 880

Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala
885 890 895

Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp
900 905 910

Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg
915 920 925

Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu
930 935 940

Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe
945 950 955 960

Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala
965 970 975

Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu
980 985 990

Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile
995 1000 1005

Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys
1010 1015 1020

Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly
1025 1030 1035 1040

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met
1045 1050 1055

Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu

1060	1065	1070
Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu 1075	1080	1085
Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala 1090	1095	1100
Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu 1105	1110	1115 1120
Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg 1125	1130	1135
Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn 1140	1145	1150
Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro 1155	1160	1165
Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro 1170	1175	1180
Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr 1185	1190	1195 1200
Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr 1205	1210	1215
Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly 1220	1225	1230
Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro 1235	1240	1245
Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro 1250	1255	1260
Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser 1265	1270	1275 1280
Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly 1285	1290	1295
Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser 1300	1305	1310
Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Arg 1315	1320	1325
Gly Ala Arg Ser His Asn Pro Arg Asn Pro Thr Ser Thr Ala Met Gly 1330	1335	1340
Ser Ser Val Pro Ser Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser 1345	1350	1355 1360
Ala Ser Val Thr Val Ala Val His Pro Pro Pro Gly Pro Gly Arg Asn 1365	1370	1375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Phe Phe Trp Glu Gln Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACGAATTC AARGTNCAYC ARYTNTGG

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGACGAATTC CYTCCCARAA RCANTC

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATACCAGCC AAGCTTGTCN GGCCARTGCA T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGG GACCGCAAGG AGTGCCGCGG AAGCGCCCGA AGGACAGGCT CGCTCGGCGC	60
GCCGGCTCTC GCTCTTCCGC GAACTGGATG TGGGCAGCGG CGGCCGAGA GACCTCGGGA	120
CCCCCGCGCA ATGTGGCAAT GGAAGGCGCA GGGTCTGACT CCCCAGGAGC GGCCGCGGCC	180
GCAGCGGCAG CAGCGCCCGC CGTGTGAGCA GCAGCAGCGG CTGGTCTGTC AACCAGGAGC	240
CGAGCCCGAG CAGCCTGCGG CCAGCAGCGT CCTCGCAAGC CGAGCGCCCA GGCGCGCCAG	300
GAGCCCGCAG CAGCGGCAGC AGCGCGCCCG GCGCCCGGG AAGCCTCCGT CCCCAGGCGG	360
GCGGCGGCGG CGGCGGCGGC AACATGGCCT CGGCTGGTAA CGCCGCGAG CCCCAGGACC	420
GCGGCGGCGG CGGCGGCGGC TGTATCGGTG CCCCAGGAGC GCGGCTGGA GGCGGAGGC	480
GCAGACGGAC GGGGGGGCTG CGCCGTGCTG CCGCGCCGGA CCGGGACTAT CTGCACCGGC	540
CCAGCTACTG CGAGCCCGCC TTCGCTCTGG AGCAGATTTC CAAGGGGAAG GCTACTGGCC	600
GGAAAGCGCC ACTGTGGCTG AGAGCGAAGT TTCAGAGACT CTTATTAACT CTGGGTTGTT	660
ACATTCAAAA AACTGCGGC AAGTTCTTGG TTGTGGGCCT CCTCATATTT GGGGCCTTCG	720

CGGTGGGATT	AAAAGCAGCG	AACCTCGAGA	CCAACGTGGA	GGAGCTGTGG	GTGGAAGTTG	780
GAGGACGAGT	AAGTCGTGAA	TTAAATTATA	CTCGCCAGAA	GATTGGAGAA	GAGGCTATGT	840
TTAATCCTCA	ACTCATGATA	CAGACCCCTA	AAGAAGAAGG	TGCTAATGTC	CTGACCACAG	900
AAGCGCTCCT	ACAACACCTG	GACTCGGCAC	TCCAGGCCAG	CCGTGTCCAT	GTATACATGT	960
ACAACAGGCA	GTGGAAATTG	GAACATTTGT	GTTACAAATC	AGGAGAGCTT	ATCACAGAAA	1020
CAGGTTACAT	GGATCAGATA	ATAGAATATC	TTTACCCTTG	TTTGATTATT	ACACCTTTGG	1080
ACTGCTTCTG	GGAAGGGGCG	AAATTACAGT	CTGGGACAGC	ATACCTCCTA	GGTAAACCTC	1140
CTTTGCGGTG	GACAAACTTC	GACCCTTTGG	AATTCCTGGA	AGAGTTAAAG	AAAATAAACT	1200
ATCAAGTGGA	CAGCTGGGAG	GAAATGCTGA	ATAAGGCTGA	GGTTGGTCAT	GGTTACATGG	1260
ACCGCCCCTG	CCTCAATCCG	GCCGATCCAG	ACTGCCCCGC	CACAGCCCCC	AACAAAAATT	1320
CAACCAAACC	TCTTGATATG	GCCCTTGTTT	TGAATGGTGG	ATGTCATGGC	TTATCCAGAA	1380
AGTATATGCA	CTGGCAGGAG	GAGTTGATTG	TGGGTGGCAC	AGTCAAGAAC	AGCACTGGAA	1440
AACTCGTCAG	CGCCCATGCC	CTGCAGACCA	TGTTCCAGTT	AATGACTCCC	AAGCAAATGT	1500
ACGAGCACTT	CAAGGGGTAC	GAGTATGTCT	CACACATCAA	CTGGAACGAG	GACAAAGCGG	1560
CAGCCATCCT	GGAGGCCTGG	CAGAGGACAT	ATGTGGAGGT	GGTTCATCAG	AGTGTCGCAC	1620
AGAACTCCAC	TCAAAAGGTG	CTTTCCTTCA	CCACCACGAC	CCTGGACGAC	ATCCTGAAAT	1680
CCTTCTCTGA	CGTCAGTGTC	ATCCGCGTGG	CCAGCGGCTA	CTTACTCATG	CTCGCCTATG	1740
CCTGTCTAAC	CATGCTGCGC	TGGGACTGCT	CCAAGTCCCA	GGGTGCCGTG	GGGCTGGCTG	1800
GCGTCCTGCT	GGTTGCACTG	TCAGTGGCTG	CAGGACTGGG	CCTGTGCTCA	TTGATCGGAA	1860
TTTCCTTTAA	CGCTGCAACA	ACTCAGGTTT	TGCCATTCT	CGCTCTTGGT	GTTGGTGTGG	1920
ATGATGTTTT	TCTTCTGGCC	CACGCCTTCA	GTGAAACAGG	ACAGAATAAA	AGAATCCCTT	1980
TTGAGGACAG	GACCGGGGAG	TGCCTGAAGC	GCACAGGAGC	CAGCGTGGCC	CTCACGTCCA	2040
TCAGCAATGT	CACAGCCTTC	TTCATGGCCG	CGTTAATCCC	AATTCOCGCT	CTGCGGGCGT	2100
TCTCCCTCCA	GGCAGCGGTA	GTAGTGGTGT	TCAATTTTGC	CATGGTTCTG	CTCATTTTTTC	2160
CTGCAATTCT	CAGCATGGAT	TTATATCGAC	GCGAGGACAG	GAGACTGGAT	ATTTTCTGCT	2220
GTTTTACAAG	CCCCTGCGTC	AGCAGAGTGA	TTCAGGTTGA	ACCTCAGGCC	TACACCGACA	2280
CACACGACAA	TACCCGCTAC	AGCCCCCAC	CTCCCTACAG	CAGCCACAGC	TTTGCCCATG	2340
AAACGCAGAT	TACCATGCAG	TCCACTGTCC	AGCTCCGCAC	GGAGTACGAC	CCCCACACGC	2400
ACGTGTACTA	CACCACCGCT	GAGCCGCGCT	CCGAGATCTC	TGTGCAGCCC	GTCACCGTGA	2460

CACAGGACAC	CCTCAGCTGC	CAGAGCCCAG	AGAGCACCAG	CTCCACAAGG	GACCTGCTCT	2520
CCCAGTTCTC	CGACTCCAGC	CTCCACTGCC	TCGAGCCCCC	CTGTACGAAG	TGGACACTCT	2580
CATCTTTTGC	TGAGAAGCAC	TATGCTCCTT	TCCTCTTGAA	ACCAAAAGCC	AAGGTAGTGG	2640
TGATCTTCCT	TTTTCTGGGC	TTGCTGGGGG	TCAGCCTTTA	TGGCACCACC	CGAGTGAGAG	2700
ACGGGCTGGA	CCTTACGGAC	ATTGTACCTC	GGGAAACCAG	AGAATATGAC	TTTATTGCTG	2760
CACAATTCAA	ATACTTTTCT	TTCTACAACA	TGTATATAGT	CACCCAGAAA	GCAGACTACC	2820
CGAATATCCA	GCACTTACTT	TACGACCTAC	ACAGGAGTTT	CAGTAACGTG	AAGTATGTCA	2880
TGTTGGAAGA	AAACAAACAG	CTTCCCAAAA	TGTGGCTGCA	CTACTTCAGA	GACTGGCTTC	2940
AGGGACTTCA	GGATGCATTT	GACAGTGA CT	GGGAAACCGG	GAAAATCATG	CCAAACAATT	3000
ACAAGAATGG	ATCAGACGAT	GGAGTCCTTG	CCTACAAACT	CCTGGTGCAA	ACCGGCAGCC	3060
GCGATAAGCC	CATCGACATC	AGCCAGTTGA	CTAAACAGCG	TCTGGTGGAT	GCAGATGGCA	3120
TCATTAATCC	CAGCGCTTTC	TACATCTACC	TGACGGCTTG	GGTCAGCAAC	GACCCCGTCG	3180
CGTATGCTGC	CTCCCAGGCC	AACATCCGGC	CACACCGACC	AGAATGGGTC	CACGACAAAG	3240
CCGACTACAT	GCCTGAAACA	AGGCTGAGAA	TCCCGGCAGC	AGAGCCCATC	GAGTATGCCC	3300
AGTTCCCTTT	CTACCTCAAC	GGGTGCGGG	ACACCTCAGA	CTTTGTGGAG	GCAATTGAAA	3360
AAGTAAGGAC	CATCTGCAGC	AACTATACGA	GCCTGGGGCT	GTCCAGTTAC	CCCAACGGCT	3420
ACCCCTTCCT	CTTCTGGGAG	CAGTACATCG	GCCTCCGCCA	CTGGCTGCTG	CTGTTCATCA	3480
GCGTGGTGTT	GGCCTGCACA	TTCCTCGTGT	GCGCTGTCTT	CCTTCTGAAC	CCCTGGACGG	3540
CCGGGATCAT	TGTGATGGTC	CTGGCGCTGA	TGACGGTCGA	GCTGTTCCGC	ATGATGGGCC	3600
TCATCGGAAT	CAAGCTCAGT	GCCGTGCCCC	TGGTCATCCT	GATCGCTTCT	GTTGGCATAG	3660
GAGTGGAGTT	CACCGTTCAC	GTTGCTTTGG	CCTTTCTGAC	GGCCATCGGC	GACAAGAACC	3720
GCAGGGCTGT	GCTTGCCCTG	GAGCACATGT	TTGCACCCGT	CCTGGATGGC	GCCGTGTCCA	3780
CTCTGCTGGG	AGTGCTGATG	CTGGCGGGAT	CTGAGTTCGA	CTTCATTGTC	AGGTATTTCT	3840
TTGCTGTGCT	GGCGATCCTC	ACCATCCTCG	GCGTTCTCAA	TGGGCTGGTT	TTGCTTCCCG	3900
TGCTTTTGTC	TTTCTTTGGA	CCATATCCTG	AGGTGTCTCC	AGCCAACGGC	TTGAACCGCC	3960
TGCCCCACAC	CTCCCCTGAG	CCACCCCCCA	GCGTGGTCCG	CTTCGCCATG	CCGCCCCGCC	4020
ACACGCACAG	CGGGTCTGAT	TCCTCCGACT	CGGAGTATAG	TTCCCAGACG	ACAGTGTCAG	4080
GCCTCAGCGA	GGAGCTTCGG	CACTACGAGG	CCCAGCAGGG	CGCGGGAGGC	CCTGCCCCACC	4140
AAGTGATCGT	GGAAGCCACA	GAAAACCCCG	TCTTCGCCCA	CTCCACTGTG	GTCCATCCCG	4200

AATCCAGGCA TCACCCACCC TCGAACCCGA GACAGCAGCC CCACCTGGAC TCAGGGTCCC 4260
 TGCCTCCCGG ACGGCAAGGC CAGCAGCCCC GCAGGGACCC CCCCAGAGAA GGCTTGTGGC 4320
 CACCCCTCTA CAGACCGCGC AGAGACGCTT TTGAAATTTC TACTGAAGGG CATTCTGGCC 4380
 CTAGCAATAG GGCCCGCTGG GGCCCTCGCG GGGCCCGTTC TCACAACCCT CGGAACCCAG 4440
 CGTCCACTGC CATGGGCAGC TCCGTGCCCC GCTACTGCCA GCCCATCACC ACTGTGACGG 4500
 CTTCTGCCTC CGTGA CTGTC GCCGTGCACC CGCCGCCTGT CCCTGGGCCT GGGCGGAACC 4560
 CCCGAGGGGG ACTCTGCCCA GGCTACCCTG AGACTGACCA CGGCCTGTTT GAGGACCCCC 4620
 ACGTGCCTTT CCACGTCCGG TGTGAGAGGA GGGATTCGAA GGTGGAAGTC ATTGAGCTGC 4680
 AGGACGTGGA ATGCGAGGAG AGGCCCCGGG GAAGCAGCTC CAACTGAGGG TGATTAAAAT 4740
 CTGAAGCAAA GAGGCCAAAG ATTGGAAACC CCCACCCCC ACCTCTTTCC AGAACTGCTT 4800
 GAAGAGAACT GGTGGAGTT ATGAAAAGA TGCCCTGTGC CAGGACAGCA GTTCATTGTT 4860
 ACTGTAACCG ATTGTATTAT TTTGTAAAT ATTTCTATAA ATATTTAAGA GATGTACACA 4920
 TGTGTAATAT AGGAAGGAAG GATGTAAAGT GGTATGATCT GGGGCTTCTC CACTCCTGCC 4980
 CCAGAGTGTG GAGGCCACAG TGGGGCCTCT CCGTATTGT GCATTGGGCT CCGTGCCACA 5040
 ACCAAGCTTC ATTAGTCTTA AATTCAGCA TATGTTGCTG CTGCTTAAAT ATTGTATAAT 5100
 TTA CTGTAT AATTCTATGC AAATATTGCT TATGTAATAG GATTATTTTG TAAAGGTTTC 5160
 TGTTTAAAT ATTTAAATT TGCATATCAC AACCCTGTGG TAGTATGAAA TGTTACTGTT 5220
 AACTTTCAA CACGTATGC GTGATAATTT TTTTGTTTAA TGAGCAGATA TGAAGAAAGC 5280
 CCGGAATT 5288

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly Gly
 1 5 10 15
 Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly Gly Arg
 20 25 30

Arg Arg Arg Thr Gly Gly Leu Arg Arg Ala Ala Ala Pro Asp Arg Asp	35	40	45
Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu Glu Gln	50	55	60
Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp Leu Arg	65	70	75
Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile Gln Lys	85	90	95
Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly Ala Phe	100	105	110
Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu Glu Leu	115	120	125
Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr Thr Arg	130	135	140
Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met Ile Gln	145	150	155
Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu	165	170	175
Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met	180	185	190
Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser Gly Glu	195	200	205
Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr Leu Tyr	210	215	220
Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys	225	230	235
Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg Trp	245	250	255
Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys Ile Asn	260	265	270
Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu Val Gly	275	280	285
His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro Asp Cys	290	295	300
Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp Met Ala	305	310	315
Leu Val Leu Asn Gly Gly Cys His Gly Leu Ser Arg Lys Tyr Met His	325	330	335
Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ser Thr Gly			

340										345										350										
Lys	Leu	Val	Ser	Ala	His	Ala	Leu	Gln	Thr	Met	Phe	Gln	Leu	Met	Thr															
355										360										365										
Pro	Lys	Gln	Met	Tyr	Glu	His	Phe	Lys	Gly	Tyr	Glu	Tyr	Val	Ser	His															
370										375										380										
Ile	Asn	Trp	Asn	Glu	Asp	Lys	Ala	Ala	Ala	Ile	Leu	Glu	Ala	Trp	Gln															
385										390										395										
Arg	Thr	Tyr	Val	Glu	Val	Val	His	Gln	Ser	Val	Ala	Gln	Asn	Ser	Thr															
405										410										415										
Gln	Lys	Val	Leu	Ser	Phe	Thr	Thr	Thr	Thr	Leu	Asp	Asp	Ile	Leu	Lys															
420										425										430										
Ser	Phe	Ser	Asp	Val	Ser	Val	Ile	Arg	Val	Ala	Ser	Gly	Tyr	Leu	Leu															
435										440										445										
Met	Leu	Ala	Tyr	Ala	Cys	Leu	Thr	Met	Leu	Arg	Trp	Asp	Cys	Ser	Lys															
450										455										460										
Ser	Gln	Gly	Ala	Val	Gly	Leu	Ala	Gly	Val	Leu	Leu	Val	Ala	Leu	Ser															
465										470										475										
Val	Ala	Ala	Gly	Leu	Gly	Leu	Cys	Ser	Leu	Ile	Gly	Ile	Ser	Phe	Asn															
485										490										495										
Ala	Ala	Thr	Thr	Gln	Val	Leu	Pro	Phe	Leu	Ala	Leu	Gly	Val	Gly	Val															
500										505										510										
Asp	Asp	Val	Phe	Leu	Leu	Ala	His	Ala	Phe	Ser	Glu	Thr	Gly	Gln	Asn															
515										520										525										
Lys	Arg	Ile	Pro	Phe	Glu	Asp	Arg	Thr	Gly	Glu	Cys	Leu	Lys	Arg	Thr															
530										535										540										
Gly	Ala	Ser	Val	Ala	Leu	Thr	Ser	Ile	Ser	Asn	Val	Thr	Ala	Phe	Phe															
545										550										555										
Met	Ala	Ala	Leu	Ile	Pro	Ile	Pro	Ala	Leu	Arg	Ala	Phe	Ser	Leu	Gln															
565										570										575										
Ala	Ala	Val	Val	Val	Val	Phe	Asn	Phe	Ala	Met	Val	Leu	Leu	Ile	Phe															
580										585										590										
Pro	Ala	Ile	Leu	Ser	Met	Asp	Leu	Tyr	Arg	Arg	Glu	Asp	Arg	Arg	Leu															
595										600										605										
Asp	Ile	Phe	Cys	Cys	Phe	Thr	Ser	Pro	Cys	Val	Ser	Arg	Val	Ile	Gln															
610										615										620										
Val	Glu	Pro	Gln	Ala	Tyr	Thr	Asp	Thr	His	Asp	Asn	Thr	Arg	Tyr	Ser															
625										630										635										
Pro	Pro	Pro	Pro	Tyr	Ser	Ser	His	Ser	Phe	Ala	His	Glu	Thr	Gln	Ile															
645										650										655										

Thr	Met	Gln	Ser	Thr	Val	Gln	Leu	Arg	Thr	Glu	Tyr	Asp	Pro	His	Thr	
			660					665					670			
His	Val	Tyr	Tyr	Thr	Thr	Ala	Glu	Pro	Arg	Ser	Glu	Ile	Ser	Val	Gln	
		675					680					685				
Pro	Val	Thr	Val	Thr	Gln	Asp	Thr	Leu	Ser	Cys	Gln	Ser	Pro	Glu	Ser	
		690				695					700					
Thr	Ser	Ser	Thr	Arg	Asp	Leu	Leu	Ser	Gln	Phe	Ser	Asp	Ser	Ser	Leu	
705					710					715					720	
His	Cys	Leu	Glu	Pro	Pro	Cys	Thr	Lys	Trp	Thr	Leu	Ser	Ser	Phe	Ala	
				725					730					735		
Glu	Lys	His	Tyr	Ala	Pro	Phe	Leu	Leu	Lys	Pro	Lys	Ala	Lys	Val	Val	
			740					745					750			
Val	Ile	Phe	Leu	Phe	Leu	Gly	Leu	Leu	Gly	Val	Ser	Leu	Tyr	Gly	Thr	
		755					760						765			
Thr	Arg	Val	Arg	Asp	Gly	Leu	Asp	Leu	Thr	Asp	Ile	Val	Pro	Arg	Glu	
	770					775					780					
Thr	Arg	Glu	Tyr	Asp	Phe	Ile	Ala	Ala	Gln	Phe	Lys	Tyr	Phe	Ser	Phe	
785					790					795					800	
Tyr	Asn	Met	Tyr	Ile	Val	Thr	Gln	Lys	Ala	Asp	Tyr	Pro	Asn	Ile	Gln	
				805					810					815		
His	Leu	Leu	Tyr	Asp	Leu	His	Arg	Ser	Phe	Ser	Asn	Val	Lys	Tyr	Val	
			820					825					830			
Met	Leu	Glu	Glu	Asn	Lys	Gln	Leu	Pro	Lys	Met	Trp	Leu	His	Tyr	Phe	
		835					840					845				
Arg	Asp	Trp	Leu	Gln	Gly	Leu	Gln	Asp	Ala	Phe	Asp	Ser	Asp	Trp	Glu	
	850					855					860					
Thr	Gly	Lys	Ile	Met	Pro	Asn	Asn	Tyr	Lys	Asn	Gly	Ser	Asp	Asp	Gly	
865					870					875					880	
Val	Leu	Ala	Tyr	Lys	Leu	Leu	Val	Gln	Thr	Gly	Ser	Arg	Asp	Lys	Pro	
				885					890					895		
Ile	Asp	Ile	Ser	Gln	Leu	Thr	Lys	Gln	Arg	Leu	Val	Asp	Ala	Asp	Gly	
			900					905					910			
Ile	Ile	Asn	Pro	Ser	Ala	Phe	Tyr	Ile	Tyr	Leu	Thr	Ala	Trp	Val	Ser	
		915					920					925				
Asn	Asp	Pro	Val	Ala	Tyr	Ala	Ala	Ser	Gln	Ala	Asn	Ile	Arg	Pro	His	
		930				935					940					
Arg	Pro	Glu	Trp	Val	His	Asp	Lys	Ala	Asp	Tyr	Met	Pro	Glu	Thr	Arg	
945					950					955					960	
Leu	Arg	Ile	Pro	Ala	Ala	Glu	Pro	Ile	Glu	Tyr	Ala	Gln	Phe	Pro	Phe	

Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu
 980 985 990
 Lys Val Arg Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser
 995 1000 1005
 Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu
 1010 1015 1020
 Arg His Trp Leu Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe
 1025 1030 1035 1040
 Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile Ile
 1045 1050 1055
 Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met Met Gly
 1060 1065 1070
 Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu Ile Ala
 1075 1080 1085
 Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu Ala Phe
 1090 1095 1100
 Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala Val Leu Ala Leu Glu
 1105 1110 1115 1120
 His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu Leu Gly
 1125 1130 1135
 Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg Tyr Phe
 1140 1145 1150
 Phe Ala Val Leu Ala Ile Leu Thr Ile Leu Gly Val Leu Asn Gly Leu
 1155 1160 1165
 Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Tyr Pro Glu Val
 1170 1175 1180
 Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro
 1185 1190 1195 1200
 Pro Pro Ser Val Val Arg Phe Ala Met Pro Pro Gly His Thr His Ser
 1205 1210 1215
 Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser
 1220 1225 1230
 Gly Leu Ser Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly
 1235 1240 1245
 Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe
 1250 1255 1260
 Ala His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser
 1265 1270 1275 1280

Asn Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly		
1285	1290	1295
Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly Leu Trp		
1300	1305	1310
Pro Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser Thr Glu		
1315	1320	1325
Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly Pro Arg Gly Ala		
1330	1335	1340
Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr Ala Met Gly Ser Ser		
1345	1350	1355 1360
Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser Ala Ser		
1365	1370	1375
Val Thr Val Ala Val His Pro Pro Pro Val Pro Gly Pro Gly Arg Asn		
1380	1385	1390
Pro Arg Gly Gly Leu Cys Pro Gly Tyr Pro Glu Thr Asp His Gly Leu		
1395	1400	1405
Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu Arg Arg Asp		
1410	1415	1420
Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys Glu Glu Arg		
1425	1430	1435 1440
Pro Arg Gly Ser Ser Ser Asn		
1445		